

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CAR §1.821 - §1.825 for the following reasons(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 CAR §1.821 - §1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990, and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CAR §1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CAR §1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CAR §1.822 and/or §1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing".
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CAR §1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CAR §1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**APPLICANT MUST PROVIDE:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as were as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CAR §1.821(e) or §1.821(f) or §1.821(g) or §1.825(b) or §1.825(d).

**FOR QUESTIONS REGARDING COMPLIANCE WITH THESE REQUIREMENTS, PLEASE CONTACT:**

For Rules Interpretation, call (703) 308-1123  
For CRF Submission help, call (703)308-4212  
For Patent Software help, call (703) 557-0400

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE.**



1645

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/446,677

DATE: 09/06/2000  
TIME: 11:01:37

Input Set : A:\Birkell.txt  
Output Set: N:\CRF3\09062000\I446677.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:  
5 (i) APPLICANT: BIRKELUND, Svend  
6 CHRISTIANSEN, Gunna  
7 HEBBSGAARD PEDERSEN, Anna-Sofie  
8 MYGIND, Per  
9 KNUDSEN, Katrine  
11 (ii) TITLE OF INVENTION: SURFACE EXPOSED PROTEINS FROM CHLAMYDIA  
12 PNEUMONIAE  
14 (iii) NUMBER OF SEQUENCES: 30  
16 (iv) CORRESPONDENCE ADDRESS:  
17 (A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
18 (B) STREET: 624 Ninth Street, N.W., Suite 300  
19 (C) CITY: Washington  
20 (D) STATE: D.C.  
21 (E) COUNTRY: USA  
22 (F) ZIP: 20001  
24 (v) COMPUTER READABLE FORM:  
25 (A) MEDIUM TYPE: Floppy disk  
26 (B) COMPUTER: IBM PC compatible  
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
30 (vi) CURRENT APPLICATION DATA:  
C--> 31 (A) APPLICATION NUMBER: US/09/446,677  
C--> 32 (B) FILING DATE: 24-Mar-2000  
C--> 38 (vii) PRIOR APPLICATION DATA:  
35 (A) APPLICATION NUMBER: PCT/DK98/00266  
36 (B) FILING DATE: 19-JUN-1998  
39 (A) APPLICATION NUMBER: DK 0744/97  
40 (B) FILING DATE: 23-JUN-1997  
42 (viii) ATTORNEY/AGENT INFORMATION:  
43 (A) NAME: COOPER, Iver P.  
44 (B) REGISTRATION NUMBER: 28,005  
45 (C) REFERENCE/DOCKET NUMBER: BIRKELUND=1  
47 (ix) TELECOMMUNICATION INFORMATION:  
48 (A) TELEPHONE: 202-628-5197  
49 (B) TELEFAX: 202-737-3528

Does Not Comply  
Corrected Diskette Needed

See pp. 2, 4, 6

## ERRORED SEQUENCES

498 (2) INFORMATION FOR SEQ ID NO: 3:  
500 (i) SEQUENCE CHARACTERISTICS:  
501 (A) LENGTH: 2815 base pairs  
502 (B) TYPE: nucleic acid  
503 (C) STRANDEDNESS: single  
504 (D) TOPOLOGY: linear

RAW SEQUENCE LISTING  
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Enter "hard return"  
here to correct.

506 (ii) MOLECULE TYPE: Genomic DNA  
508 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
E--> 510  
ATGAAATCGC AATTTTCCTG GTTAGTGCTC TCTTCGACAT TGGCATGTTT TACTAGTTGT 60 TCCACTGTTT TTGCTGCAAC TGCTGAAAT ATA  
511 ACTAACACAG GCACCTATAC TCCTAAAAAT ACGACTACTG GAATAGACTA TACTCTGACA 180  
512 GGAGATATAA CTCTGCAAAA CCTTGGGGAT TCGGCAGCTT TAACGAAGGG TTGTTTTTCT 240  
513 GACACTACGG AATCTTTAAG CTTTGCCGGT AAGGGGTACT CACTTTCTTT TTTAAATATT 300  
514 AAGTCTAGTG CTGAAGGCGC AGCACTTTCT GTTACAACCT ATAAAAATCT GTCGCTAACA 360  
515 GGATTTTCGA GTCTTACTTT CTTAGCGGCC CCATCATCGG TAATCACAAC CCCCTCAGGA 420  
516 AAAGGTGCAG TTAATGTGGG AGGGGATCTT ACATTGATA ACAATGGAAC TATTTTATTT 480  
517 AAACAAGATT ACTGTGAGGA AAATGGCGGA GCCATTCTA CCAAGAATCT TTCTTTGAAA 540  
518 AACAGCAGCG GATCGATTTC TTTTGAAGGG AATAAATCGA GCGCAACAGG GAAAAAAGGT 600  
519 GGGGCTATTT GTGCTACTGG TACTGTAGAT ATTACAAATA ATACGGCTCC TACCCCTCTC 660  
520 TCGAACAAATA TTGCTAAGC TGCAGGTGGA GCTATAAATA GCACAGGAAA CTGTACAATT 720  
521 ACAGGGAATA CGTCTCTTGT ATTTTCTGAA AATAGTGTGA CAGCGACCGC AGGAAATGGA 780  
522 GGAGCTCTTT CTGGAGATGC CGATGTTACC ATATCTGGGA ATCAGAGTGT AACTTTCTCA 840  
523 GGAACCAAG CTGTAGCTAA TGGCGGAGCC ATTTATGCTA AGAAGCTTAC ACTGGCTTCC 900  
524 GGGGGGGGGG GGGGTATCTC CTTTCTAAC AATATAGTCC AAGGTACCA TGCAGGTAAT 960  
525 GGTGGAGCCA TTTCTATACT GGCAGCTGGA GAGTGTAGTC TTTCAGCAGA AGCAGGGGAC 1020  
526 ATTACCTTCA ATGGGAATGC CATTTGTTGA ACTACACCA AACTACAAA AAGAAATCT 1080  
527 ATTGACATAG GATCTACTGC AAAGATCAGC AATTATCGTG CAATATCTGG GCATAGCATC 1140  
528 TTTTCTACG ATCCGATTAC TGCTAATACG GCTGCGGATT CTACAGATAC TTTAAATCTC 1200  
529 AATAAGGCTG ATGCAGGTAA TAGTACAGAT TATAGTGGGT CGATTGTTTT TTCTGGTGAA 1260  
530 AAGCTCTCTG AAGATGAAGC AAAAGTTGCA GACAACCTCA CTTCTACGCT GAAGCAGCCT 1320  
531 GTAACCTTAA CTGCAGGAAA TTTAGTACTT AAACGTGGTG TCACTCTCGA TACGAAAGGC 1380  
532 TTTACTCAGA CCGCGGGTTC CTCTGTTAT ATGGATGCGG GCACAACGTT AAAAGCAAGT 1440  
533 ACAGAGGAGG TCACTTTAAC AGGTCTTTCC ATTCCTGTAG ACTCTTTAGG CGAGGGTAAG 1500  
534 AAAGTTGTAA TTGCTGCTTC TGCAGCAAGT AAAAAATGAG CCCTTAGTGG TCCGATTCTT 1560  
535 CTTTGGGATA ACCAAGGGAA TGCTTATGAA AATCAGGACT TAGGAAAAAC TCAAGACTTT 1620  
536 TCATTTGTGC AGCTCTCTGC TCTGGGTACT GCAACAATA CAGATGTTCC AGCGGTTCCT 1680  
537 ACAGTAGCAA CTCCTACGCA CTATGGGTAT CAAGGTACTT GGGGAATGAC TTGGGTGAT 1740  
538 GATACCGCAA GCACTCCAAA GACTAAGACA GCGACATTAG CTTGGACCAA TACAGGCTAC 1800  
539 CTTCCGAATC CTGAGCGTCA AGGACCTTTA GTTCCTAATA GCCTTTGGGG ATCTTTTCA 1860  
540 GACATCCAAG CGATTCAAGG TGTCATAGAG AGAAGTGCTT TGAATCTTTG TTCAGATCGA 1920  
541 GGCTTCTGGG CTGCGGGAGT CGCCAATTTT TTAGATAAAG ATAAGAAAGG GGAAGAACGC 1980  
542 AAATACCGTC ATAAATCTGG TGGATATGCT ATCGGAGGTG CAGCGCAAAC TTGTTCTGAA 2040  
543 AACTTAATTA GCTTTGCTTT TGGCAACTC TTTGGTAGCG ATAAAGATTT CTTAGTCGCT 2100  
544 AAAAAATCAT CTGATACCTA TGCAGGAGCC TTCTATATCC AACACATTAC AGAATGTAGT 2160  
545 GGGTTTCATG GTTGCTCTCT AGATAAACTT CCTGGCTCTT GGAGTCATAA ACCCCTCGTT 2220  
546 TTAGAAGGGC AGCTCGCTTA TAGCCACGTC AGTAATGATC TGAAGACAAA GTATACTGCG 2280  
547 TATCTTGAGG TGAAGGTTT TTGGGGGAAT AATGCTTTTA ACATGATGTT GGGAGCTTCT 2340  
548 TCTCATTTCT ATCCTGAATA CCTGCATTGT TTTGATACCT ATGCTCCATA CATCAAACTG 2400  
549 AATCTGACCT ATATACGTCA GGACAGCTTC TCGGAGAAAG GTACAGAAGG AAGATCTTTT 2460  
550 GATGACAGCA ACCTCTTCAA TTTATCTTTG CCTATAGGGG TGAAGTTTGA GAAGTCTCT 2520  
551 GATTGTAATG ACTTTTCTTA TGATCTGACT TTATCCTATG TTCCTGATCT TATCCGCAAT 2580  
552 GATCCCAAAT GCACTACAGC ACTTGTAAAT AGCGGAGCCT CTTGGGAAAC TTATGCCAAT 2640  
553 AACTTAGCAC GACAGGCCTT GCAAGTGCCT ACTACGCCTT CTCTCCTATG 2700  
554 TTTGAAGTGC TCGGCCAGTT TGTCTTTGAA GTTCGTGGAT CCTCAGGAT TTATAATGTA 2760  
555 GATCTTGGGG GTAAGTTCCA ATTCTAGGAG CGTCTCTCAT GTCTCAGAAA TTCTG 2815  
743 (2) INFORMATION FOR SEQ ID NO: 5:

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/446,677

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Input Set : A:\Birkell.txt  
Output Set: N:\CRF3\09062000\I446677.raw

745 (i) SEQUENCE CHARACTERISTICS:  
746 (A) LENGTH: 3052 base pairs → see p. 4  
747 (B) TYPE: nucleic acid  
748 (C) STRANDEDNESS: single  
749 (D) TOPOLOGY: linear  
751 (ii) MOLECULE TYPE: Genomic DNA  
753 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
755 ATGCGATTTC CGCTCTGCGG ATTTCCTCTA GTTTTCTCTT TAACATTGCT CTCAGTCTTC 60  
756 GACACTTCTT TGAGTGCTAC TACGATTCTT TTAACCCAG AAGATAGTT TCATGGAGAT 120  
757 AGTCAGAAATG CAGAACGTTT TTATAATGTT CAAGCTGGGG ATGTCTATAG CCTTACTGGT 180  
758 GATGTCTCAA TATCTAACGT CGATAACTCT GCATTAAATA AAGCCTGCTT CAATGTGACC 240  
759 TCAGGAAGTG TGACGTTTCG AGGAAATCAT CATGGGTTAT ATTTTAATAA GGCACGTTT 300  
760 GGAAGTACAA AGGAAGGGGG TGTACTTTGT TGCCAAGATC CTCAGCAAC ACAGGGATGT 360  
761 TCTGGGTTCT CCACGCTCTC TTTTATTCAG AGCCCGGAG ATATTAAAGA ACAGGGATGT 420  
762 CTCTATTCAA AAAATGCACT TATGCTCTTA AACAAATTAT TAGTGCCTTT TGAACAAAAC 480  
763 CAAAGTAAGA CTAAGAGCGG AGCTATTAGT GGGGCGAATG TTAATAAGT AGGCAACTAC 540  
764 GATTCCGTCT CTTTCTATCA GAATGCAGCC ACTTTTGGAG GTGCTATCCA TTCTTCAGGT 600  
765 CCCCTACAGA TTGCAGTAAA TCAGGCAGAG ATAAGATTG CACAAAATAC TGCCAAGAAT 660  
766 GGTCTCTGAG GGGCTTTGTA CTCCGATGGT GATATTGATA TTGATCAGAA TGCTTATGTT 720  
767 CTATTTCGAG AAAATGAGGC ATTGACTACT GCTATAGGTA AGGGAGGGGG TGCTTGTGTT 780  
768 CTTCCCACTT CAGGAAGTAG TACTCCAGTT CCTATTGTGA CTTTCTCTGA CAATAAACAG 840  
769 TTAGTCTTTG AAAGAAACCA TTCCATAATG GGTGGCGGAG CCATTATGTC TAGGAACTT 900  
770 AGCATCTCTT CAGGAGGTCC TACTCTATTT ATCAATAATA TATCATATGC AAATTCGCAA 960  
771 AATTAGGTG GAGCTATTGC CATTGATACT GGAGGGGAGA TCAGTTTATC AGCAGAGAAA 1020  
772 GGAACAATTA CATTCCAAGG AAACCGGACG AGCTTACCGT TTTTGAATGG CATCCATCTT 1080  
773 TTACAAAATG CTTCTGAAGC AGATGGGTCT ACCCAATTGA ATATCAACGG AGATCCTAAA 1140  
774 GATCCTATTA CTAAATTCCT GAAATTACAG GCGAGAAATG GATGCTCTAT AGAATTTTAT 1200  
775 AATAAAGAGT ACACAGGGAC CATACTCTTT TCTGGAGAAA AGAGTCTAGC AAACGATCCT 1260  
776 AGGGATTTTA AATCTACAAT CCCTCAGAAC GTCACCTGT CTGCAGGATA CTTAGTTATT 1320  
777 AAAGAGGGGG CCGAAGTCAC AGTTTCAAAA TTCACGCAGT CTCCAGGATC GCATTTAGTT 1380  
778 TTAGATTTAG GAACCAAACT GATAGCCTCT AAGGAAGACA TTGCCATCAC AGGCCTCGCG 1440  
779 ATAGATATAG ATAGCTTAAG CTCATCCTCA ACAGCAGCTG TTATTAAAGC AAACACGCA 1500  
780 AATAAACAGA TATCCGTGAC GGACTCTATA GAACTTATCT CGCCTACTGG CAATGCCTAT 1560  
781 GAAGATCTCA GAATGAGAAA TTCACAGACG TTCCCTCTGC TCTCTTTAGA GCCTGGAGCC 1620  
782 GGGGGTAGTG TGACTGTAAC TGCTGGAGAT TTCCTACCGG TAAGTCCCA TTATGGTTT 1680  
783 CAAGGCAATT GGAATTAGC TTGGACAGGA ACTGGAACA AAGTTGGAGA ATTCTTCTGG 1740  
784 GATAAAATAA ATTATAAGCC TAGACCTGAA AAAGAAGGAA ATTTAGTTCC TAATATCTTG 1800  
785 TGGGGGAATG CTGTAAATGT CAGATCCTTA ATGCAGGTTT AAGAGACCCA TGCAATCGAGC 1860  
786 TTACAGACAG ATCGAGGGCT GTGGATCGAT GGAATTGGGA ATTTCTTCCA TGTATCTGCC 1920  
787 TCCGAAGACA ATATAAGGTA CCGTCATAAC AGCGGTGGAT ATGTCTATC TGTAATAAT 1980  
788 GAGATCACAC CTAAGCACTA TACTTCGATG GCATTTTCCC AACTCTTTAG TAGAGACAAG 2040  
789 GACTATGCGG TTTCCAACAA CGAATACAGA ATGTATTAG GATCGTATCT CTATCAATAT 2100  
790 ACAACCTCCC TAGGGAATAT TTTCCGTTAT GCTTCGCGTA ACCCTAATGT AAACGTCGGG 2160  
791 ATTCTCTCAA GAAGGTTTCT TCAAAATCCT CTTATGATTT TTCATTTTTT GTGTGCTTAT 2220  
792 GGTCAATGCC CCAATGATAT GAAAAACAGC TACGCAAAAT TCCCTATGGT GAAAAACAGC 2280  
793 TGGAGAAACA ATTGTTGGGC TATAGAGTGC GGAGGGAGCA TGCCCTTATT GGTATTGAG 2340  
794 AACGGAAGAC TTTTCCAAGG TGCCATCCCA TTTATGAAAC TACAAATTAG TTATGCTTAT 2400  
795 CAGGGAGATT TCAAGAGAC GACTGCAGAT GGCCGTAGAT TTAGTAATGG GAGTTTAAAC 2460  
796 TCGATTTCGT TACCTCTAGG CATACGCTTT GAGAAGCTGG CACTTCTCA GGATGTAATC 2520

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/446,677

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797 TATGACTTTA GTTCTCCTA TATTCCTGAT ATTTCCCGTA AGGATCCCTC ATGTGAAGCT 2580  
798 GCTCTGGTGA TTACCGGAGA CTCCTGGCTT GTTCCGGCAG CACACGTATC AAGACATGCT 2640  
799 TTTGTAGGGA GTGGAACGGG TCGGTATCAC TTTAACGACT ATACTGAGCT CTTATGTCGA 2700  
800 GGAAGTATAG AATGCCGCCC CCATGCTAGG AATTATAATA TAACTGTGG AAGCAAATTT 2760  
801 CGTTTTTAGA AGGTTTCCAT TGCCTGTGTG GTTCCGGATC TTAACATAAA ATCCTGGACT 2820  
802 ATGGATCATA GGCATTGGGT TTCTCGAAT TGTGTGGAGA ATAACGACAT TTTATATGCA 2880  
803 TAACGGAATA CTCGTATCAC CTCAGCCCCT AGAGACATTC TTTAGGGGTT CTTTATTGT 2940  
804 CTAAACTTCG TATTTATCG AGAATCCTTT ACGTTCCTGG TTTGCTTGTC TCCGAGGAGT 3000  
E--> 805 TCTCTAACGA ATCATAGGGA TTCCAGGGTT CTGTTCTCTG AGTCCTTTGG A 3052

2597 (2) INFORMATION FOR SEQ ID NO: 24:  
2599 (i) SEQUENCE CHARACTERISTICS:  
2600 (A) LENGTH: 246 amino acids  
2601 (B) TYPE: amino acid  
2602 (C) STRANDEDNESS: single  
2603 (D) TOPOLOGY: linear  
2605 (ii) MOLECULE TYPE: peptide  
2607 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
2609 Met Lys Thr Ser Val Ser Met Leu Leu Ala Leu Cys Ser Gly Ala  
2610 1 5 10 15  
2612 Ser Ser Ile Val Leu His Ala Ala Thr Thr Pro Leu Asn Pro Glu Asp  
2613 20 25 30  
2615 Gly Phe Ile Gly Glu Gly Asn Thr Asn Thr Phe Ser Pro Lys Ser Thr  
2616 35 40 45  
2618 Thr Asp Ala Ala Gly Thr Thr Tyr Ser Leu Thr Gly Glu Val Leu Phe  
2619 50 55 60  
2621 Ile Asp Pro Gly Lys Gly Ser Ile Thr Gly Thr Cys Phe Val Glu  
2622 65 70 75 80  
2624 Thr Ala Gly Asp Leu Thr Phe Leu Gly Asn Gly Asn Thr Leu Lys Phe  
2625 85 90 95  
2627 Leu Ser Val Asp Ala Gly Ala Asn Ile Ala Val Ala His Val Gln Gly  
2628 100 105 110  
2630 Ser Lys Asn Leu Ser Phe Thr Asp Phe Leu Ser Leu Val Ile Thr Glu  
2631 115 120 125  
2633 Ser Pro Lys Ser Ala Val Ser Thr Gly Lys Gly Ser Leu Val Ser Ser  
2634 130 135 140  
2636 Gly Ala Val Gln Leu Gln Asp Ile Asn Thr Leu Val Leu Thr Ser Asn  
2637 145 150 155 160  
2639 Ala Ser Val Glu Asp Gly Gly Val Ile Lys Gly Asn Ser Cys Leu Ile  
2640 165 170 175  
2642 Gln Gly Ile Lys Asn Ser Ala Ile Phe Gly Gln Asn Thr Ser Ser Lys  
2643 180 185 190  
2645 Lys Gly Gly Ala Ile Ser Thr Thr Gln Gly Leu Thr Ile Glu Asn Asn  
2646 195 200 205  
2648 Leu Gly Thr Leu Lys Phe Asn Glu Asn Lys Ala Val Thr Ser Gly Gly  
2649 210 215 220  
2651 Ala Leu Asp Leu Gly Ala Ala Ser Thr Phe Thr Ala Asn His Glu Leu  
2652 225 230 235 240  
2654 Ile Phe Ser Gln Asn Lys Thr Ser Gly Asn Ala Ala Asn Gly Gly Ala  
2655 245 250 255

Number of bases  
conflict, 3052  
listed, 3051 four

→ See p. 6

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 PATENT APPLICATION: US/09/446,677

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Input Set : A:\Birkell.txt  
 Output Set: N:\CRF3\09062000\I446677.raw

2657 Ile Asn Cys Ser Gly Asp Leu Thr Phe Thr Asp Asn Thr Ser Leu Leu  
 2658 260 265 270  
 2660 Leu Gln Glu Asn Ser Thr Met Gln Asp Gly Gly Ala Leu Cys Ser Thr  
 2661 275 280 285  
 2663 Gly Thr Ile Ser Ile Thr Gly Ser Asp Ser Ile Asn Val Ile Gly Asn  
 2664 290 295 300  
 2666 Thr Ser Gly Gln Lys Gly Gly Ala Ile Ser Ala Ala Ser Leu Lys Ile  
 2667 305 310 315 320  
 2669 Leu Gly Gly Gln Gly Gly Ala Leu Phe Ser Asn Asn Val Val Thr His  
 2670 325 330 335  
 2672 Ala Thr Pro Leu Gly Gly Ala Ile Phe Ile Asn Thr Gly Gly Ser Leu  
 2673 340 345 350  
 2675 Gln Leu Phe Thr Gln Gly Gly Asp Ile Val Phe Glu Gly Asn Gln Val  
 2676 355 360 365  
 2678 Thr Thr Thr Ala Pro Asn Ala Thr Thr Lys Arg Asn Val Ile His Leu  
 2679 370 375 380  
 2681 Glu Ser Thr Ala Lys Trp Thr Gly Leu Ala Ala Ser Gln Gly Asn Ala  
 2682 385 390 395 400  
 2684 Ile Tyr Phe Tyr Asp Pro Ile Thr Thr Asn Asp Thr Gly Ala Ser Asp  
 2685 405 410 415  
 2687 Asn Leu Arg Ile Asn Glu Val Ser Ala Asn Gln Lys Leu Ser Gly Ser  
 2688 420 425 430  
 2690 Ile Val Phe Ser Gly Glu Arg Leu Ser Thr Ala Glu Ala Ile Ala Glu  
 2691 435 440 445  
 2693 Asn Leu Thr Ser Arg Ile Asn Gln Pro Val Thr Leu Val Glu Gly Ser  
 2694 450 455 460  
 2696 Leu Glu Leu Lys Gln Gly Val Thr Leu Ile Thr Gln Gly Phe Ser Gln  
 2697 465 470 475 480  
 2699 Glu Pro Glu Ser Thr Leu Leu Leu Asp Leu Gly Thr Ser Leu Gln Ala  
 2700 485 490 495  
 2702 Ser Thr Glu Asp Ile Val Ile Thr Asn Ser Ser Ile Asn Ala Asp Thr  
 2703 500 505 510  
 2705 Ile Tyr Gly Lys Asn Pro Ile Asn Ile Val Ala Ser Ala Ala Asn Lys  
 2706 515 520 525  
 2708 Asn Ile Thr Leu Thr Gly Thr Leu Ala Leu Val Asn Ala Asp Gly Ala  
 2709 530 535 540  
 2711 Leu Tyr Glu Asn His Thr Leu Gln Asp Ser Gln Asp Tyr Ser Phe Val  
 2712 545 550 555 560  
 2714 Lys Leu Ser Pro Gly Ala Gly Gly Thr Ile Ile Thr Gln Asp Ala Ser  
 2715 565 570 575  
 2717 Gln Lys Leu Leu Glu Val Ala Pro Ser Arg Pro His Tyr Gly Tyr Gln  
 2718 580 585 590  
 2720 Gly His Trp Asn Val Gln Val Ile Pro Gly Thr Gly Thr Gln Pro Ser  
 2721 595 600 605  
 2723 Gln Ala Asn Leu Glu Trp Val Arg Thr Gly Tyr Leu Pro Asn Pro Glu  
 2724 610 615 620  
 2726 Arg Gln Gly Phe Leu Val Pro Asn Ser Leu Trp Gly Ser Phe Val Asp  
 2727 625 630 635 640  
 2729 Gln Arg Ala Ile Gln Glu Ile Met Val Asn Ser Ser Gln Ile Leu Cys

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2730 645 650 655  
2732 Gln Glu Arg Gly Val Trp Gly Ala Gly Ile Ala Asn Phe Leu His Arg  
2733 660 665 670  
2735 Asp Lys Ile Asn Glu His Gly Tyr Arg His Ser Gly Val Gly Tyr Leu  
2736 675 680 685  
2738 Val Gly Val Gly Thr His Ala Phe Ser Asp Ala Thr Ile Asn Ala Ala  
2739 690 695 700  
2741 Phe Cys Gln Leu Phe Ser Arg Asp Lys Asp Tyr Val Val Ser Lys Asn  
2742 705 710 715 720  
2744 His Gly Thr Ser Tyr Ser Gly Val Val Phe Leu Glu Asp Thr Leu Glu  
2745 725 730 735  
2747 Phe Arg Ser Pro Gln Gly Phe Tyr Thr Asp Ser Ser Ser Glu Ala Cys  
2748 740 745 750  
2750 Cys Asn Gln Val Val Thr Ile Asp Met Gln Leu Ser-Tyr Ser His Arg  
2751 755 760 765  
2753 Asn Asn Asp Met Lys Thr Lys Tyr Thr Thr Tyr Pro Glu Ala Gln Gly  
2754 770 775 780  
2756 Ser Trp Ala Asn Asp Val Phe Gly Leu Glu Phe Gly Ala Thr Thr Tyr  
2757 785 790 795 800  
2759 Tyr Tyr Pro Asn Ser Thr Phe Leu Phe Asp Tyr Tyr Ser Pro Phe Leu  
2760 805 810 815  
2762 Arg Leu Gln Cys Thr Tyr Ala His Gln Glu Asp Phe Lys Glu Thr Gly  
2763 820 825 830  
2765 Gly Glu Val Arg His Phe Thr Ser Gly Asp Leu Phe Asn Leu Ala Val  
2766 835 840 845  
2768 Pro Ile Gly Val Lys Phe Glu Arg Phe Ser Asp Cys Lys Arg Gly Ser  
2769 850 855 860  
2771 Tyr Glu Leu Thr Leu Ala Tyr Val Pro Asp Val Ile Arg Lys Asp Pro  
2772 865 870 875 880  
2774 Lys Ser Thr Ala Thr Leu Ala Ser Gly Ala Thr Trp Ser Thr His Gly  
2775 885 890 895  
2777 Asn Asn Leu Ser Arg Gln Gly Leu Gln Leu Arg Leu Gly Asn His Cys  
2778 900 905 910  
2780 Leu Ile Asn Pro Gly Ile Glu Val Phe Ser His Gly Ala Ile Glu Leu  
2781 915 920 925  
2783 Arg Gly Ser Ser Arg Asn Tyr Asn Ile Asn Leu Gly Gly Lys Tyr Arg  
2784 930 935 940  
2786 Phe  
E---> 2787 945

→ 945 amino acids found, 946 listed as length.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/446,677

DATE: 09/06/2000  
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Input Set : A:\Birkell.txt  
Output Set: N:\CRF3\09062000\I446677.raw

L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:38 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:510 M:320 E: (1) Wrong Nucleic Acid Designator, 2  
L:805 M:254 E: No. of Bases conflict, Input:3052 Counted:3051 SEQ:5  
L:805 M:204 E: No. of Bases differ, LENGTH:Input:3052 Counted:3051 SEQ:5  
L:2454 M:220 C: Keyword misspelled or invalid format, [(ii) MOLECULE TYPE:]  
L:2787 M:203 E: No. of Seq. differs, LENGTH:Input:946 Found:945 SEQ:24